

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

- (i) APPLICANT: Iverson, Brent  
Georgiou, George  
Chen, Gang  
Olsen, Mark J.  
Daugherty, Patrick S.
- (ii) TITLE OF INVENTION: Directed Evolution of Enzymes and Antibodies
- (iii) NUMBER OF SEQUENCES: 53
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: ARNOLD, WHITE AND DURKEE
  - (B) STREET: P.O. Box 4433
  - (C) CITY: Houston
  - (D) STATE: Texas
  - (E) COUNTRY: USA
  - (F) ZIP: 77210-4433
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US UNKNOWN
  - (B) FILING DATE: CONCURRENTLY HEREWITH
  - (C) CLASSIFICATION: UNKNOWN
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Highlander, Steven L.
  - (B) REGISTRATION NUMBER: 37,642
  - (C) REFERENCE/DOCKET NUMBER: UTSB620
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (512) 418-3000
  - (B) TELEFAX: (713) 789-2679

### (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 780 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..780

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GAA | GTT | CAA | CTG | CAA | CAG | TCT | GGT | CCT | GAA | TTG | GTT | AAA | CCT | GGC | GGC | 48  |
| Glu | Val | Gln | Leu | Gln | Gln | Ser | Gly | Pro | Glu | Leu | Val | Lys | Pro | Gly | Ala |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |     |
| TCT | GTG | CGC | ATG | TCC | TGC | AAA | TCC | TCA | GGG | TAC | ATT | TTC | ACC | GAC | TTC | 96  |
| Ser | Val | Arg | Met | Ser | Cys | Ser | Ser | Gly | Tyr | Ile | Phe | Thr | Asp | Phe |     |     |
| 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |     |     |
| TAC | ATG | AAT | TGG | GTT | CGC | CAG | TCT | CAT | GGT | AAG | TCT | CTA | GAC | TAC | ATC | 144 |
| Tyr | Met | Asn | Trp | Val | Arg | Gln | Ser | His | Gly | Lys | Ser | Leu | Asp | Tyr | Ile |     |
| 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
| GGG | TAC | ATT | TCC | CCA | TAC | TCT | GGG | GTT | ACC | GGC | TAC | AAC | CAG | AAG | TTT | 192 |
| Gly | Tyr | Ile | Ser | Pro | Tyr | Ser | Gly | Val | Thr | Gly | Tyr | Asn | Gln | Lys | Phe |     |
| 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| AAA | GGT | AAG | GCC | ACC | CTT | ACT | GTC | GAC | AAA | TCT | TCC | TCA | ACT | GCT | TAC | 240 |
| Lys | Gly | Lys | Ala | Thr | Leu | Thr | Val | Asp | Lys | Ser | Ser | Ser | Thr | Ala | Tyr |     |
| 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |     |
| ATG | GAG | CTG | CGT | TCT | TTG | ACC | TCT | GAG | GAC | TCC | GCG | GTA | TAC | TAT | TGC | 288 |
| Met | Glu | Leu | Arg | Ser | Leu | Thr | Ser | Glu | Asp | Ser | Ala | Val | Tyr | Tyr | Cys |     |
| 85  |     |     |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |     |
| GCC | GGC | TCC | TCT | GGT | AAC | AAA | TGG | GCC | ATG | GAT | TAT | TGG | GGT | CAT | GGT | 336 |
| Ala | Gly | Ser | Ser | Gly | Asn | Lys | Trp | Ala | Met | Asp | Tyr | Trp | Gly | His | Gly |     |
| 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |     |     |
| GCT | AGC | GTT | ACT | GTG | AGC | TCT | GGT | GGC | GGC | TCG | GGC | GGT | GGT | GGG | 384 |     |
| Ala | Ser | Val | Thr | Val | Ser | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Gly |     |
| 115 |     |     |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |     |
| TCG | GGT | GGC | GGC | GGA | TCA | GAC | ATA | GTA | CTG | ACC | CAG | TCT | CCA | GCT | TCT | 432 |
| Ser | Gly | Gly | Gly | Ser | Asp | Ile | Val | Leu | Thr | Gln | Ser | Pro | Ala | Ser |     |     |
| 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |     |
| TTG | GCT | GTG | TCT | CTA | GGA | CAA | AGG | GCC | ACG | ATA | TCC | TGC | CGA | TCC | AGC | 480 |
| Leu | Ala | Val | Ser | Leu | Gly | Gln | Arg | Ala | Thr | Ile | Ser | Cys | Arg | Ser | Ser |     |
| 145 |     |     |     |     |     | 150 |     |     |     | 155 |     |     | 160 |     |     |     |
| CAA | AGT | CTC | GTA | CAT | TCT | AAT | GGT | AAT | ACT | TAT | CTG | AAC | TGG | TAC | CAA | 528 |
| Gln | Ser | Leu | Val | His | Ser | Asn | Gly | Asn | Thr | Tyr | Leu | Asn | Trp | Tyr | Gln |     |
| 165 |     |     |     |     |     |     | 170 |     |     |     | 175 |     |     |     |     |     |
| CAG | AAA | CCA | GGA | CAG | CCA | CCC | AAG | CTT | CTC | ATC | TAT | AAG | GTA | TCC | AAC | 576 |
| Gln | Lys | Pro | Gly | Gln | Pro | Pro | Lys | Leu | Leu | Ile | Tyr | Lys | Val | Ser | Asn |     |
| 180 |     |     |     |     |     |     | 185 |     |     |     | 190 |     |     |     |     |     |
| CGA | TTC | TCT | GGA | GTC | CCT | GCC | AGG | TTC | AGT | GGC | AGT | GGG | TCT | GAG | TCA | 624 |
| Arg | Phe | Ser | Gly | Val | Pro | Ala | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Glu | Ser |     |
| 195 |     |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |     |     |
| GAC | TTC | ACC | CTC | ACC | ATC | GAT | CCT | GTG | GAG | GAA | GAT | GAT | GCT | GCA | ATA | 672 |
| Asp | Phe | Thr | Leu | Thr | Ile | Asp | Pro | Val | Glu | Glu | Asp | Asp | Ala | Ala | Ile |     |
| 210 |     |     |     |     |     | 215 |     |     |     | 220 |     |     |     |     |     |     |

|   |     |
|---|-----|
| TAT TAC TGT AGC CAA ACT ACG CAT GTT CCA CCC ACG TTC GGC TCG GGG | 720 |
| Tyr Tyr Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Ser Gly |     |
| 225 230 235 240   |     |
| ACC AAG CTG GAG CTG AAA CGT GCT AGC CAG CCA GAA CTC GCC CCG GAA | 768 |
| Thr Lys Leu Glu Leu Lys Arg Ala Ser Gln Pro Glu Leu Ala Pro Glu |     |
| 245 250 255   |     |
| GAC CCC GAG GAC   | 780 |
| Asp Pro Glu Asp   |     |
| 260   |     |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|   |  |
|---|--|
| Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala |  |
| 1 5 10 15   |  |
| Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp Phe |  |
| 20 25 30  |  |
| Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr Ile |  |
| 35 40 45  |  |
| Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys Phe |  |
| 50 55 60  |  |
| Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr |  |
| 65 70 75 80   |  |
| Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys |  |
| 85 90 95  |  |
| Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His Gly |  |
| 100 105 110   |  |
| Ala Ser Val Thr Val Ser Ser Gly Gly Ser Gly Gly Gly Gly Gly     |  |
| 115 120 125   |  |
| Ser Gly Gly Gly Ser Asp Ile Val Leu Thr Gln Ser Pro Ala Ser     |  |
| 130 135 140   |  |
| Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Arg Ser Ser |  |
| 145 150 155 160   |  |
| Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Gln |  |
| 165 170 175   |  |
| Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn |  |
| 180 185 190   |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Phe | Ser | Gly | Val | Pro | Ala | Arg | Phe | Ser | Gly | Ser | Gly | Ser | Glu | Ser |
| 195 |     |     |     |     |     |     | 200 |     |     |     |     |     |     | 205 |     |
| Asp | Phe | Thr | Leu | Thr | Ile | Asp | Pro | Val | Glu | Glu | Asp | Asp | Ala | Ala | Ile |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Tyr | Tyr | Cys | Ser | Gln | Thr | Thr | His | Val | Pro | Pro | Thr | Phe | Gly | Ser | Gly |
| 225 |     |     |     |     |     | 230 |     |     | 235 |     |     | 240 |     |     |     |
| Thr | Lys | Leu | Glu | Leu | Lys | Arg | Ala | Ser | Gln | Pro | Glu | Leu | Ala | Pro | Glu |
|     |     |     |     |     | 245 |     |     | 250 |     |     |     | 255 |     |     |     |
| Asp | Pro | Glu | Asp |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 260 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGGACCAACA ACATCGGT

18

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCATATCAC CAGCTCACCG TCTTTC

26

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACCCCGAGG ACTAACGTCT TCGAATAAAT AC

32

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGAATTCGT TTGAACATGC CTAAC

25

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGGAATTCGT GCGAACACCG ATGAAGCTC

29

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGGGCATGCA AGGGCACCAA TAACTGCCTT A

31

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTGGCTGCAG TAATATATTG CAGCAT

26

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGCAATATAT TACTGCAGCC AAACTACGCA T

31

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGGCAGTTTC TGCAGATATA TTCGCAAGAT

30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CTTGCAGATA TATCTGCAGA AACTGCCGGA A

31

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACGCCACATC TTGCGAATAT ATCTGCAGAA ACTGCCGGAA

40

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAGGGTACAT TTTCACCG

18

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: one-of(13, 14, 22, 23, 28, 29)
- (D) OTHER INFORMATION: /note= "N = A, C, T or G"

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: one-of(15, 24, 30)
- (D) OTHER INFORMATION: /note= "B = C, G or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AACTGCAGCC AANNBACGCA TNNBCCANNB ACGTTCGGCT CGGGGA

46

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: one-of(31, 32, 34, 35, 37, 38, 40, 41)
- (D) OTHER INFORMATION: /note= "N = A, C, T or G"

(ix) FEATURE:

- (A) NAME/KEY: modified\_base
- (B) LOCATION: one-of(33, 36, 39, 42)
- (D) OTHER INFORMATION: /note= "S = C or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTATACTATT GCGCCGGCTC CTCTGGTAAC NNSNNNSNNSN NSGATTATTG GGGTCATGGT

60

GCT

63

(2) INFORMATION FOR SEQ ID NO:17:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTTACCAAGAG GAGCCGGCGC AATAGTATAC

30

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TACATTTCA CCGACTTCAA TATGAATTGG GTTCGC

36

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TACATTTCA CCGACTTCTG CATGAATTGG GTTCGC

36

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TACATTTCA CCGACTTCTC TATGAATTGG GTTCGC

36

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TACATTTCA CCGACTTCGG GATGAATTGG GTTCGC

36

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TACATTTCA CCGACTTCTA AATGAATTGG GTTCGC

36

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ser Gln Thr Thr His Val Pro Pro Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Gln Ala Thr His Met Pro Gly Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ser Gln Thr Thr His Phe Pro Val Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ser Gln Ala Thr His Tyr Pro Thr Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Gln Cys Thr His Trp Pro Val Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Gln Thr Thr His Val Pro Pro Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ser Gln Ala Thr His Tyr Pro Ser Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ser Gln Ala Thr His Ser Pro Ser Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ser Gln Val Thr His Gly Pro Arg Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ser Gln Gly Thr His Arg Pro Tyr Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ser Gln Ile Thr His Val Pro Lys Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Gln Leu Thr His Leu Pro Arg Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ser Gln Pro Thr His Val Pro Pro Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Gln Val Thr His Lys Pro Gly Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ser Gln Leu Thr His Trp Pro Ser Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ser Gln Leu Thr His Gly Pro Arg Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Gln Leu Thr His Gly Pro Arg Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Ser Gln Glx Thr His Gly Pro Phe Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ser Ser Gly Asn Tyr Arg Ala Leu Asp Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Ser Gly Asn Arg Arg Ala Trp Asp Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ser Ser Gly Asn Arg Arg Ala Leu Asp Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ser Ser Gly Asn Gly Arg Ala Trp Asp Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ser Ser Gly Asn Ile Ser Ala Leu Asp Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ser Ser Gly Asn Gln Arg Lys Met Asp Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Gln Thr Thr His Val Pro Pro Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser Gln Val Thr His Arg Pro Leu Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Ser Gln Val Thr His Asp Pro Gly Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Ser Gln Val Thr His Cys Pro Ser Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser Gln Val Thr His Trp Pro Pro Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:53:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ser Gln Val Thr His Tyr Pro Val Thr  
1 5